Phyre²

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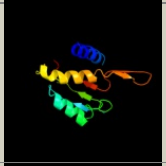
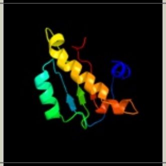
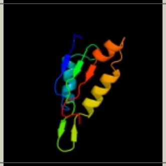
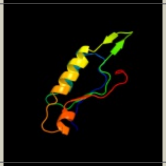
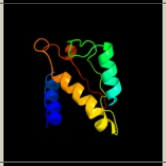
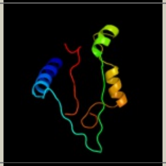
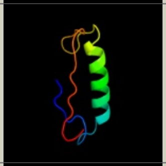
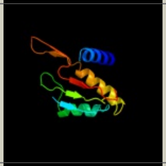
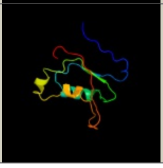
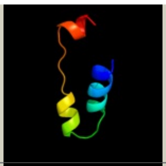
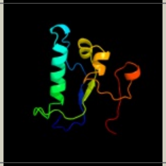
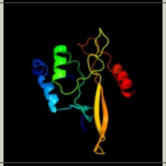
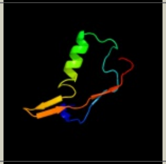
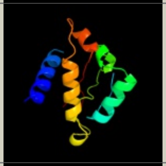
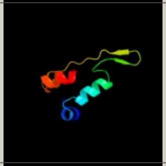
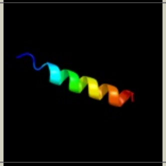
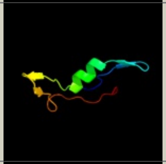
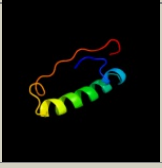
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3c5wc1	Alignment		73.4	21	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
2	d1jk7a_	Alignment		59.2	21	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
3	d2p6ba1	Alignment		52.1	28	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
4	c2p6bC_	Alignment		51.7	28	**PDB header:**hydrolase/hydrolase regulator **Chain:** C: **PDB Molecule:**calmodulin-dependent calcineurin a subunit alpha **PDBTitle:** crystal structure of human calcineurin in complex with2 pvivit peptide
5	c1auiA_	Alignment		49.5	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine/threonine phosphatase 2b; **PDBTitle:** human calcineurin heterodimer
6	d1auia_	Alignment		49.5	35	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
7	d1s70a_	Alignment		45.0	24	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
8	d1s95a_	Alignment		42.7	24	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
9	c2zbmA_	Alignment		42.7	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein-tyrosine-phosphatase; **PDBTitle:** crystal structure of i115m mutant cold-active protein2 tyrosine phosphatase
10	c3icfB_	Alignment		39.1	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine/threonine-protein phosphatase t; **PDBTitle:** structure of protein serine/threonine phosphatase from saccharomyces2 cerevisiae with similarity to human phosphatase pp5
11	c2qjcA_	Alignment		33.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diadenosine tetraphosphatase, putative; **PDBTitle:** crystal structure of a putative diadenosine tetraphosphatase

12	c2dfjA_	Alignment		31.1	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diadenosinetetraphosphatase; **PDBTitle:** crystal structure of the diadenosine tetraphosphate2 hydrolase from shigella flexneri 2a
13	d2nxfa1	Alignment		28.9	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**ADPRibase-Mn-like
14	c1oidA_	Alignment		28.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein usha; **PDBTitle:** 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c)
15	d1ii7a_	Alignment		24.1	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DNA double-strand break repair nuclease
16	c2jogA_	Alignment		23.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**calmodulin-dependent calcineurin a subunit alpha **PDBTitle:** structure of the calcineurin-nfat complex
17	c2wdfA_	Alignment		22.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sulfur oxidation protein soxb; **PDBTitle:** termus thermophilus sulfate thiohydrolase soxb
18	c1p0oA_	Alignment		22.6	32	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** hp (2-20) substitution of trp for gln and asp at position2 17 and 19 modification in sds-d25 micelles
19	c1wao4_	Alignment		22.5	41	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**serine/threonine protein phosphatase 5; **PDBTitle:** pp5 structure
20	d1uf3a_	Alignment		20.4	8	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
21	c2kkrA_	Alignment	not modelled	19.4	29	**PDB header:**transcription, protein binding **Chain:** A: **PDB Molecule:**ataxin-7; **PDBTitle:** solution structure of sca7 zinc finger domain from human ataxin-72 protein
22	d1xm7a_	Alignment	not modelled	15.0	22	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Hypothetical protein aq 1666
23	d1qfxa_	Alignment	not modelled	14.6	12	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
24	d1pv8a_	Alignment	not modelled	13.6	43	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
25	c2aklA_	Alignment	not modelled	13.2	53	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phna-like protein pa0128; **PDBTitle:** solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
26	c3alxB_	Alignment	not modelled	13.2	24	**PDB header:**viral protein/membrane protein **Chain:** B: **PDB Molecule:**hemagglutinin, cdw150; **PDBTitle:** crystal structure of the measles virus hemagglutinin bound to its2 cellular receptor slam (mv-h(l482r)-slam(n102h/r108y) fusion)
27	d2akka1	Alignment	not modelled	13.0	47	**Fold:**SH3-like barrel **Superfamily:**Prokaryotic SH3-related domain **Family:**PhnA-like
28	d1qcsa2	Alignment	not modelled	12.6	25	**Fold:**Cdc48 domain 2-like **Superfamily:**Cdc48 domain 2-like **Family:**Cdc48 domain 2-like

29	d2q4ma1	Alignment	not modelled	12.5	22	**Fold:**Tubby C-terminal domain-like **Superfamily:**Tubby C-terminal domain-like **Family:**At5g01750-like
30	c1zxuA_	Alignment	not modelled	12.5	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**at5g01750 protein; **PDBTitle:** x-ray structure of protein from arabidopsis thaliana2 at5g01750
31	d2akla1	Alignment	not modelled	12.5	53	**Fold:**SH3-like barrel **Superfamily:**Prokaryotic SH3-related domain **Family:**PhnA-like
32	c2jwlB_	Alignment	not modelled	11.7	27	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**protein tolr; **PDBTitle:** solution structure of periplasmic domain of tolr from h.2 influenzae with saxs data
33	d1s04a_	Alignment	not modelled	11.4	20	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
34	c3av0A_	Alignment	not modelled	11.3	26	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11-rad50 bound to atp s
35	c2k2bA_	Alignment	not modelled	11.3	64	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**degenerin mec-4; **PDBTitle:** sparse-constraint solution nmr structure of micelle-2 solublized cytosolic amino terminal domain of c. elegans3 mechanosensory ion channel subunit mec-4. new york4 consortium on membrane protein structure (nycomps) (casp5 target)
36	d2z1aa2	Alignment	not modelled	11.0	18	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
37	c2eqxA_	Alignment	not modelled	10.6	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**kelch repeat and btb domain-containing protein 4; **PDBTitle:** solution structure of the back domain of kelch repeat and2 btb domain-containing protein 4
38	c3auzA_	Alignment	not modelled	10.3	26	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11 with manganese
39	d1g5ba_	Alignment	not modelled	9.5	26	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
40	d1myna_	Alignment	not modelled	9.1	58	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Insect defensins
41	c3letB_	Alignment	not modelled	8.6	53	**PDB header:**transferase **Chain:** B: **PDB Molecule:**adenosine monophosphate-protein transferase vops; **PDBTitle:** crystal structure of fic domain containing ampylator, vops
42	c1s3mA_	Alignment	not modelled	8.3	28	**PDB header:**phosphodiesterase **Chain:** A: **PDB Molecule:**hypothetical protein mj0936; **PDBTitle:** structural and functional characterization of a novel2 archaeal phosphodiesterase
43	d1s3la_	Alignment	not modelled	8.3	28	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
44	c2hb0B_	Alignment	not modelled	7.4	36	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**cfa/i fimbrial subunit e; **PDBTitle:** crystal structure of cfae, the adhesive subunit of cfa/i2 fimbria of enterotoxigenic escherichia coli
45	c2vvxA_	Alignment	not modelled	6.7	16	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein a52; **PDBTitle:** structure of vaccinia virus protein a52
46	c3ps0C_	Alignment	not modelled	6.7	26	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**crispr-associated protein, csa2; **PDBTitle:** the structure of the crispr-associated protein, csa2, from sulfolobus2 solfataricus
47	d1p42a2	Alignment	not modelled	6.7	31	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC
48	c3qfkA_	Alignment	not modelled	6.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** 2.05 angstrom crystal structure of putative 5'-nucleotidase from2 staphylococcus aureus in complex with alpha-ketoglutarate
49	c3f83A_	Alignment	not modelled	6.5	36	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**fusion of the minor pilin cfae and major pilin cfab; **PDBTitle:** structure of fusion complex of the minor pilin cfae and major pilin2 cfab of cfa/i pili from etec e. coli
50	c3lybC_	Alignment	not modelled	6.4	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative endoribonuclease; **PDBTitle:** structure of putative endoribonuclease(kp1_3112) from2 klebsiella pneumoniae
51	c3c9fB_	Alignment	not modelled	6.3	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**5'-nucleotidase; **PDBTitle:** crystal structure of 5'-nucleotidase from candida albicans sc5314
52	c3zu0A_	Alignment	not modelled	6.2	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nad nucleotidase; **PDBTitle:** structure of haemophilus influenzae nad nucleotidase (nadn)
53	c2vxdA_	Alignment	not modelled	6.2	46	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nucleophosmin; **PDBTitle:** the structure of the c-terminal domain of nucleophosmin

54	c2dbhA_	Alignment	not modelled	6.2	38	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor superfamily **PDBTitle:** solution structure of the carboxyl-terminal card-like2 domain in human tnfr-related death receptor-6
55	c3fvyA_	Alignment	not modelled	6.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl-peptidase 3; **PDBTitle:** crystal structure of human dipeptidyl peptidase iii
56	d1uoya_	Alignment	not modelled	6.1	64	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Bubble protein **Family:**Bubble protein
57	d1cr5a2	Alignment	not modelled	6.0	30	**Fold:**Cdc48 domain 2-like **Superfamily:**Cdc48 domain 2-like **Family:**Cdc48 domain 2-like
58	d1xnea_	Alignment	not modelled	5.9	11	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
59	d2f9zc1	Alignment	not modelled	5.8	40	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**CheD-like
60	c2xmoB_	Alignment	not modelled	5.7	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2642 protein; **PDBTitle:** the crystal structure of lmo2642
61	c2jgwA_	Alignment	not modelled	5.7	25	**PDB header:**immune response **Chain:** A: **PDB Molecule:**complement factor h; **PDBTitle:** structure of ccp module 7 of complement factor h - the amd2 at risk varient (402h)
62	c2ftcB_	Alignment	not modelled	5.6	17	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**mitochondrial ribosomal protein l2; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
63	c1z8yO_	Alignment	not modelled	5.6	50	**PDB header:**virus **Chain:** O: **PDB Molecule:**spike glycoprotein e1; **PDBTitle:** mapping the e2 glycoprotein of alphaviruses
64	c1z8yM_	Alignment	not modelled	5.6	50	**PDB header:**virus **Chain:** M: **PDB Molecule:**spike glycoprotein e1; **PDBTitle:** mapping the e2 glycoprotein of alphaviruses
65	c1z8yK_	Alignment	not modelled	5.6	50	**PDB header:**virus **Chain:** K: **PDB Molecule:**spike glycoprotein e1; **PDBTitle:** mapping the e2 glycoprotein of alphaviruses
66	c1z8yI_	Alignment	not modelled	5.6	50	**PDB header:**virus **Chain:** I: **PDB Molecule:**spike glycoprotein e1; **PDBTitle:** mapping the e2 glycoprotein of alphaviruses
67	d1g40a2	Alignment	not modelled	5.4	38	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
68	c2o42B_	Alignment	not modelled	5.4	34	**PDB header:**apoptosis inhibitor **Chain:** B: **PDB Molecule:**m11l protein; **PDBTitle:** crystal structure of m11l, bcl-2 homolog from myxoma virus
69	d1hcca_	Alignment	not modelled	5.3	25	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
70	c1hccA_	Alignment	not modelled	5.3	25	**PDB header:**glycoprotein **Chain:** A: **PDB Molecule:**16th complement control protein; **PDBTitle:** three-dimensional structure of a complement control protein2 module in solution
71	d1twda_	Alignment	not modelled	5.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**CutC-like **Family:**CutC-like
72	c4a1aM_	Alignment	not modelled	5.2	15	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**60s ribosomal protein l5; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.